AMENDMENT

In the Claims:

The listing of claims will replace all prior versions, and listings, of claims in the application.

1. [Previously Amended] A method of making a mixture of variable number tandem repeat (VNTR) alleles and their flanking regions of the genomic DNA of one or more members of a species of interest, which method comprises the steps of:

a) dividing genomic DNA of the species of interest into fragments,

b) ligating to each end of each fragment an adapter thereby forming a mixture of adaptor-terminated fragments in which each 3'-end is blocked to prevent enzymatic chain extension,

c) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR primer wherein said portion of the mixture of adaptor terminated fragments serves as a template to create a mixture of 5'-flanking VNTR amplimers;

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d) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR antisense primer wherein said portion of the mixture of adaptor-terminated fragments serves as template to create a mixture of 3'-flanking VNTR amplimers,

e) and producing a desired mixture of VNTR alleles and their flanking regions by contacting genomic DNA of the one or more members of the species of interest with the mixture of 5'-flanking VNTR amplimers and/or the mixture of 3'-flanking VNTR amplimers as primers wherein said genomic DNA of the one or more members of the species of interest is used as template.

2. [Original] The method of claim 1, wherein step b) is performed by terminating each 3'-end of each fragment to prevent enzymatic chain extension, and ligating each 5'-end of each fragment to an adaptor, thereby forming a mixture of adaptor terminated fragments.

3. [Previously Amended] The method of claim 1, wherein in step c) the VNTR repeat sequences are removed from the 5'-flanking VNTR amplimers, and in step d) the VNTR repeat sequences are removed from the 3'-flanking VNTR amplimers.

4. [Previously amended] The method of claim 1, wherein in step c) and/or d) at least one adaptor or primer used contains at least one phosphorothioate bond.

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5. [Previously amended] The method of claim 1, wherein step e) is performed using as primers, successively or together, both the mixture of 5'-flanking VNTR amplimers and the mixture of 3'-flanking VNTR amplimers.

6. [Previously amended] The method of claim 1, wherein there is used in step e) genomic DNA of one or more members of the species of interest which manifest a trait of interest, whereby the resulting mixture of VNTR alleles and their flanking sequences is representative of those which manifest the trait of interest.

7. [Original] The method of claim 6 wherein in a step f) the strands of the mixture of VNTR alleles and their flanking regions are separated and then re-annealed and any mis-matches are separated and discarded.

8. [Original] The method of claim 7, wherein step f) is repeated to recover a single VNTR allele and its flanking regions.

9. [Previously amended] The method of claim 6, wherein at least one VNTR allele and its flanking sequences representative of those which manifest the trait of interest, is hybridised with a mixture of VNTR alleles and their flanking sequences representative of alleles which do not manifest the trait of interest, and at least one match and/or at least one mis-match is selected to provide at least one VNTR allele or fragment thereof which is characteristic of the trait of interest.

10. [Original] The method of claim 9, wherein the at least one VNTR allele and its flanking sequences representative of those which manifest the trait of interest, is provided with 3'-overlapping ends.

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11. [Thrice Amended] A mixture of one or more VNTR alleles and their flanking regions, said mixture consisting essentially of a representative mixture of alleles of a chosen variable number tandem repeat (VNTR) sequence and their flanking regions on both sides, wherein each member of the representative mixture of alleles ~~misture of alleses~~ has an adaptor at each of its 3'-end and its 5'-end.

12. [Previously Amended] The mixture of one or more VNTR alleles and their flanking regions of claim 11, wherein the mixture of alleles is representative of those which manifest a trait of interest.

13. [Cancelled]

14. [Previously Amended] A composition consisting essentially of one or more copies of a single variable number tandem repeat (VNTR) allele and its flanking regions and an adaptor at each of its 3'-end and its 5'-end, said allele being characteristic of those which manifest a trait of interest.

15. [Four-times Amended] A mixture of VNTR flanking sequences, said mixture consisting essentially of a representative mixture of 3'-flanking regions of a chosen variable number tandem repeat (VNTR) sequence, each member of the mixture carrying an adaptor at its 3'-end and lacking 5'-flanking region, and a representative mixture of 5'-flanking regions of a chosen VNTR sequence, each member of the mixture carrying the same adaptor at its 5'-end and lacking 3'-flanking region.

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16. [Amended] A method of treating a mixture of nucleic acids, [which] the mixture consisting essentially of [a mixture of] polymorphic alleles[, the mixture being] representative of those which manifest a trait of interest, which method comprises separating and then re-annealing strands of the mixture, and separating and discarding any mis-matches.

17. [Previously Amended] The method of claim 16, wherein the mixture of polymorphic alleles is a mixture of alleles of a chosen variable number tandem repeat (VNTR) sequence and their flanking regions.

18. [Original] The method of claim 17, wherein the method is repeated to recover a single VNTR allele and its flanking regions.

19. [Four-times Amended] The method of claim 17, wherein at least one VNTR allele and its flanking sequence representative of alleles which manifest the trait of interest[,] is hybridised with a mixture of VNTR alleles and their flanking sequences representative of those which do not manifest the trait of interest, and at least one match and/or at least one mis-match is selected to provide at least one VNTR allele or fragment thereof which is characteristic of the trait of interest.

20. [Previously Amended] The method of claim 19, wherein the at least one VNTR allele and its flanking sequence representative of alleles which manifest the trait of interest, is provided with overlapping ends.

21. [Four-times Amended] A method of making a mixture of amplimers which method comprises the steps of:

a) dividing genomic DNA of one or more members of a species of interest into fragments,

b) ligating to each end of each fragment an adaptor thereby forming a mixture of adaptor-terminated fragments in which each 3'-end is blocked to prevent enzymatic chain extension, and

c) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a variable number tandem repeat (VNTR) primer wherein said portion of the mixture of adaptor-terminated fragments serves as a template to create a mixture of 5'-flanking VNTR amplimers, and/or

d) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR antisense primer wherein said portion of the

mixture of adaptor-terminated fragments serves as a template to create a mixture of 3'-flanking VNTR amplimers.

22. [Previously Amended] A method of identifying an allele which is linked to a trait of interest, which method comprises incubating together under hybridisation conditions: a composition consisting essentially of molecules of nucleic acid containing a polymorphic allele and its flanking sequences representative of those which manifest the trait of interest; and a mixture of molecules of nucleic acid which contain polymorphic alleles and their flanking sequences representative and derived from more than one of those which do not manifest the trait of interest; and selecting at least one match and/or at least one mis-match to provide at least one allele or fragment thereof which is linked to the trait of interest.

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23. [Original] The method of claim 22, wherein the alleles are VNTR alleles.

24. [Previously Amended] The method of claim 22, wherein the at least one allele and its flanking sequences representative of alleles which manifest the trait of interest, is provided with 3'-overlapping ends.

25. [Previously Amended] A method for diagnosing a trait of interest comprising the step of identifying an allele which is linked to a trait of interest according to the method of claim 22, wherein said molecules of nucleic acid are contacted with a composition consisting essentially of one or more copies of a single VNTR allele and its flanking regions and an adaptor at each of its 3'-end and its 5'-end, said allele being characteristic of those which manifest a trait of interest.

26. [Previously Amended] The method of claim 1 or claim 16, wherein the VNTR allele and its flanking regions, or the mixture of VNTR alleles and their flanking regions, is analysed by being applied under hybridisation conditions to an array of immobilised VNTR alleles and/or their flanking regions.

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27. [Previously Amended] A kit comprising protocols and reagents for performing the method of claim 1 or claim 16 or claim 24.